

RAW SEQUENCE LISTING

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Application Serial Number: 10/584,886
Source: JFWO
Date Processed by STIC: 11/09/2006

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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/584,886

DATE: 11/09/2006

TIME: 13:00:58

Input Set: N:\efs\10584886_efs\Sequence_List_176_61623.txt
 Output Set: N:\CRF4\11092006\J584886.raw

3 <110> APPLICANT: Maines, Mahin D.
 5 <120> TITLE OF INVENTION: METHODS OF MODULATING CELL CYCLE AND CELL SIGNALING PATHWAYS
 6 USING BILIVERDIN REDUCTASE
 8 <130> FILE REFERENCE: 176/61623 (1208)
 10 <140> CURRENT APPLICATION NUMBER: 10/584,886
 C--> 11 <141> CURRENT FILING DATE: 2006-06-29
 13 <150> PRIOR APPLICATION NUMBER: PCT/US2004/031866
 14 <151> PRIOR FILING DATE: 2004-09-29
 16 <150> PRIOR APPLICATION NUMBER: 60/539,006
 17 <151> PRIOR FILING DATE: 2004-01-23
 19 <150> PRIOR APPLICATION NUMBER: 60/506,805
 20 <151> PRIOR FILING DATE: 2003-09-29
 22 <160> NUMBER OF SEQ ID NOS: 7
 24 <170> SOFTWARE: PatentIn version 3.3
 26 <210> SEQ ID NO: 1
 28 <400> SEQUENCE: 1
 W--> 29 000
 31 <210> SEQ ID NO: 2
 32 <211> LENGTH: 1070
 33 <212> TYPE: DNA
 34 <213> ORGANISM: Human BVR
 36 <400> SEQUENCE: 2
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 39 atgaatgcag agcccgagag gaagtttggc gtgggtgtgg ttgggtgtgg ccgagccggc 120
 41 tccgtgcgga tgagggactt gcggaatcca caccottcct cagcgttctt gaacctgatt 180
 43 ggcttcgtgt cgagaaggaa gtcgggagc attgatggag tccagcagat ttctttggag 240
 45 gatgctcttt ccagccaaga ggtggagggtc gcctatatct gcagttagag ctccagccat 300
 47 gaggactaca tcagggcgtt cottaatgtt ggcaagcacg tccttggtga ataccccatt 360
 49 acactgtcat tggcgccgc tcaggaactg tgggagctgg ctgagcagaa aggaaaagtc 420
 51 ttgcacgagg agcatgttga actcttgatg gaggaattcg ctttccttggaa aaaagaagtg 480
 53 gtggggaaag acctgtgttga aggggtcgctc ctcttcacat ctgaccgggtt ggaagaagac 540
 55 cgggttggct tccctgcatt cagcggcattc tctcgactga cctggctgtt ctccctcttt 600
 57 ggggagcttt ctcttggttc tgccactttt gaagagcgaa aggaagatca gtatatgaaa 660
 59 atgacagtgt gtctggagac agagaagaaa agtcoactgt catggatttgaa agaaaaagga 720
 61 cctggtctaa aacgaaacag atatttaagc ttccatttca agtctgggtc cttggagaat 780
 63 gtgccaaatg taggagtgttga taagaacata tttctgtttttt atcaaaaat atttgtccag 840
 65 aaactcttgg gccagttctc tgagaaggaa ctgggtgttgc aaaagaaaacg catctgcac 900
 67 tgccctggggc ttgcagaaga aatccagaaa tattgtgtt caaggaagta agaggaggag 960
 69 gtgatgttgttgc acttccaaga tggcaccagc atttgggttct tctcaagagt tgaccattat 1020
 71 ctctatttctt aaaattaaac atgttggggaa aacaaaaaaaaaaaaaaa 1070
 74 <210> SEQ ID NO: 3
 75 <211> LENGTH: 296
 76 <212> TYPE: PRT

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77 <213> ORGANISM: Human BVR
 79 <400> SEQUENCE: 3
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 82 1 5 10 15
 85 Gly Arg Ala Gly Ser Val Arg Met Arg Asp Leu Arg Asn Pro His Pro
 86 20 25 30
 89 Ser Ser Ala Phe Leu Asn Leu Ile Gly Phe Val Ser Arg Arg Glu Leu
 90 35 40 45
 93 Gly Ser Ile Asp Gly Val Gln Gln Ile Ser Leu Glu Asp Ala Leu Ser
 94 50 55 60
 97 Ser Gln Glu Val Glu Val Ala Tyr Ile Cys Ser Glu Ser Ser His
 98 65 70 75 80
 101 Glu Asp Tyr Ile Arg Gln Phe Leu Asn Ala Gly Lys His Val Leu Val
 102 85 90 95
 105 Glu Tyr Pro Met Thr Leu Ser Leu Ala Ala Gln Glu Leu Trp Glu
 106 100 105 110
 109 Leu Ala Glu Gln Lys Gly Lys Val Leu His Glu Glu His Val Glu Leu
 110 115 120 125
 113 Leu Met Glu Glu Phe Ala Phe Leu Lys Lys Gln Val Val Gly Lys Asp
 114 130 135 140
 117 Leu Leu Lys Gly Ser Leu Leu Phe Thr Ala Gly Pro Leu Glu Glu
 118 145 150 155 160
 121 Arg Phe Gly Phe Pro Ala Phe Ser Gly Ile Ser Arg Leu Thr Trp Leu
 122 165 170 175
 125 Val Ser Leu Phe Gly Glu Leu Ser Leu Val Ser Ala Thr Leu Glu Glu
 126 180 185 190
 129 Arg Lys Glu Asp Gln Tyr Met Lys Met Thr Val Cys Leu Glu Thr Glu
 130 195 200 205
 133 Lys Lys Ser Pro Leu Ser Trp Ile Glu Glu Lys Gly Pro Gly Leu Lys
 134 210 215 220
 137 Arg Asn Arg Tyr Leu Ser Phe His Phe Lys Ser Gly Ser Leu Glu Asn
 138 225 230 235 240
 141 Val Pro Asn Val Gly Val Asn Lys Asn Ile Phe Leu Lys Asp Gln Asn
 142 245 250 255
 145 Ile Phe Val Gln Lys Leu Leu Gly Gln Phe Ser Glu Lys Glu Leu Ala
 146 260 265 270
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 150 275 280 285
 153 Gln Lys Tyr Cys Cys Ser Arg Lys
 154 290 295
 157 <210> SEQ ID NO: 4
 158 <211> LENGTH: 295
 159 <212> TYPE: PRT
 160 <213> ORGANISM: Rat BVR
 162 <400> SEQUENCE: 4
 164 Met Asp Ala Glu Pro Lys Arg Lys Phe Gly Val Val Val Val Gly Val
 165 1 5 10 15
 168 Gly Arg Ala Gly Ser Val Arg Leu Arg Asp Leu Lys Asp Pro Arg Ser
 169 20 25 30

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172 Ala Ala Phe Leu Asn Leu Ile Gly Phe Val Ser Arg Arg Glu Leu Gly
173 35 40 45
176 Ser Leu Asp Glu Val Arg Gln Ile Ser Leu Glu Asp Ala Leu Arg Ser
177 50 55 60
180 Gln Glu Ile Asp Val Ala Tyr Ile Cys Ser Glu Ser Ser Ser His Glu
181 65 70 75 80
184 Asp Tyr Ile Arg Gln Phe Leu Gln Ala Gly Lys His Val Leu Val Glu
185 85 90 95
188 Tyr Pro Met Thr Leu Ser Phe Ala Ala Gln Glu Leu Trp Glu Leu
189 100 105 110
192 Ala Ala Gln Lys Gly Arg Val Leu His Glu Glu His Val Glu Leu Leu
193 115 120 125
196 Met Glu Glu Phe Glu Phe Leu Arg Arg Glu Val Leu Gly Lys Glu Leu
197 130 135 140
200 Leu Lys Gly Ser Leu Arg Phe Thr Ala Ser Pro Leu Glu Glu Glu Arg
201 145 150 155 160
204 Phe Gly Phe Pro Ala Phe Ser Gly Ile Ser Arg Leu Thr Trp Leu Val
205 165 170 175
208 Ser Leu Phe Gly Glu Leu Ser Leu Ile Ser Ala Thr Leu Glu Glu Arg
209 180 185 190
212 Lys Glu Asp Gln Tyr Met Lys Met Thr Val Gln Leu Glu Thr Gln Asn
213 195 200 205
216 Lys Gly Leu Leu Ser Trp Ile Glu Glu Lys Gly Pro Gly Leu Lys Arg
217 210 215 220
220 Asn Arg Tyr Val Asn Phe Gln Phe Thr Ser Gly Ser Leu Glu Glu Val
221 225 230 235 240
224 Pro Ser Val Gly Val Asn Lys Asn Ile Phe Leu Lys Asp Gln Asp Ile
225 245 250 255
228 Phe Val Gln Lys Leu Leu Asp Gln Val Ser Ala Glu Asp Leu Ala Ala
229 260 265 270
232 Glu Lys Lys Arg Ile Met His Cys Leu Gly Leu Ala Ser Asp Ile Gln
233 275 280 285
236 Lys Leu Cys His Gln Lys Lys
237 290 295
240 <210> SEQ ID NO: 5
241 <211> LENGTH: 1081
242 <212> TYPE: DNA
243 <213> ORGANISM: Rat BVR
245 <400> SEQUENCE: 5
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248 aacctctgtc tgtctcgga cactgactga agagaccgag atggatgcgg agccaaagag 120
250 gaaaatttggg gtggtagtgtt gggtgtttgg cagagctggc tcggtgaggc tgagggactt 180
252 gaaggatcca cgctotgcag cattcctgaa cctgatttgg tttgtgtcca gacgagagct 240
254 tgggagcctt gatgaagtac ggcagatttc ttgtgaagat gctctccaa gccaagagat 300
256 tcatgtcgcc tatatttgca gtgagagttc cagccatgaa gactatatac ggcagttct 360
258 gcaggctggc aagcatgtcc tcgtggaaata cccccatgaca ctgtcatgg cggcgccca 420
260 ggagctgtgg gagctggccg cacagaaagg gagagtcctg catgaggagc acgtggaaact 480
262 cttgtatggag gaattcgaat tcctgagaag agaagtgttgg gggaaagagc tactgaaagg 540
264 gtctcttcgc ttcacagcta gcccactgga agaagagaga tttggcttcc ctgcgttcag 600

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268	cacccggaa	gagcgaaaag	aggatcaga	tatgaaaatg	accgtgcagc	tggagaccca		720										
270	gaacaagggt	ctgctgtcat	ggattgaaga	gaaagggcct	ggcttaaaaaa	gaaacagata		780										
272	tgtaaaacttc	cagttcaactt	ctggggtccct	ggaggaagtg	ccaagtgtag	gggtcaataa		840										
274	gaacatttc	ctgaaagatc	aggatataatt	tgttcagaag	ctcttagacc	aggctctgc		900										
276	agaggacctg	gctgtgaga	agaagcgcacat	catgcattgc	ctggggctgg	ccagcgacat		960										
278	ccagaagctt	tgccaccaga	agaagtgaag	ggaaaggcttc	agagacttct	gaagggggcc		1020										
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293	1				5				10							15		
296	Gly	Arg	Ala	Gly	Ser	Val	Arg	Ile	Arg	Asp	Ser	Lys	Asp	Pro	His	Ser		
297						20			25							30		
300	Ser	Ala	The	Ieu	Asn	Leu	Ile	Gly	Tyr	Val	Ser	Arg	Arg	Glu	Ieu	Gly		
301						35			40							45		
304	Ser	Leu	Asp	Asn	Val	Arg	Gln	Ile	Ser	Leu	Glu	Asp	Ala	Leu	Arg	Ser		
305						50			55							60		
308	Gln	Glu	Val	Asp	Val	Ala	Tyr	Ile	Cys	Thr	Glu	Ser	Ser	Ser	His	Glu		
309						65			70			75				80		
312	Asp	Tyr	Ile	Arg	Gln	Phe	Leu	Gln	Ala	Gly	Lys	His	Val	Leu	Val	Glu		
313						85			90			95						
316	Tyr	Pro	Met	Ala	Leu	Ser	Phe	Ala	Ala	Gln	Glu	Leu	Trp	Glu	Leu			
317						100			105			110						
320	Ala	Ala	Gln	Lys	Gly	Arg	Val	Leu	His	Glu	Glu	His	Ile	Glu	Leu	Leu		
321						115			120			125						
324	Met	Glu	Glu	Phe	Phe	Leu	Lys	Arg	Glu	Val	Ala	Gly	Lys	Glu	Leu			
325						130			135			140						
328	Leu	Lys	Gly	Ser	Leu	Arg	Phe	Thr	Ala	Ser	Pro	Leu	Glu	Glu	Lys			
329						145			150			155				160		
332	Phe	Gly	Phe	Pro	Ala	Phe	Ser	Gly	Ile	Ser	Arg	Leu	Thr	Trp	Leu	Val		
333						165			170			175						
336	Ser	Leu	Phe	Gly	Glu	Leu	Ser	Leu	Ile	Ser	Ala	Thr	Met	Glu	Asn	Arg		
337						180			185			190						
340	Lys	Glu	Asp	Gln	Tyr	Met	Lys	Met	Thr	Val	Gln	Leu	Glu	Thr	Gln	Asn		
341						195			200			205						
344	Lys	Ser	Pro	Leu	Ser	Trp	Ile	Glu	Glu	Lys	Gly	Pro	Gly	Leu	Lys	Arg		
345						210			215			220						
348	Asn	Arg	His	Ile	Ser	Ile	His	Phe	Lys	Ser	Gly	Ser	Leu	Glu	Glu	Val		
349						225			230			235				240		
352	Pro	Asn	Val	Gly	Val	Asn	Lys	Asn	Ile	Phe	Leu	Lys	Asp	Gln	Asp	Ile		
353						245			250			255						
356	Phe	Ile	Gln	Lys	Leu	Leu	Gly	Gln	Val	Ser	Ala	Glu	Asp	Leu	Ala	Ala		
357						260			265			270						
360	Glu	Lys	Lys	Arg	Ile	Leu	His	Cys	Leu	Glu	Leu	Ala	Ser	Asp	Ile	Gln		

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368	<210> SEQ ID NO: 7		
369	<211> LENGTH: 296		
370	<212> TYPE: PRT		
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373	<400> SEQUENCE: 7		
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376	1 5 10 15		
379	Gly Arg Ala Gly Ser Val Arg Met Arg Asp Leu Arg Asn Pro His Pro		
380	20 25 30		
383	Ser Ser Ala Phe Leu Asn Leu Ile Gly Phe Val Ser Arg Arg Glu Leu		
384	35 40 45		
387	Gly Ser Ile Asp Gly Val Gln Gln Ile Ser Leu Glu Asp Ala Leu Ser		
388	50 55 60		
391	Ser Gln Glu Val Glu Val Ala Tyr Ile Cys Ser Glu Ser Ser Ser His		
392	65 70 75 80		
395	Glu Asp T Ile Arg Gln Phe Leu Asn Ala Gly Lys His Val Leu Val		
396	85 90 95		
399	Glu Tyr Pro Met Thr Leu Ser Leu Ala Ala Ala Gln Glu Leu Trp Glu		
400	100 105 110		
403	Leu Ala Glu Gln Lys Gly Lys Val Leu His Glu Glu His Val Glu Leu		
404	115 120 125		
407	Leu Met Glu Glu Phe Ala Phe Leu Lys Glu Val Val Gly Lys Asp		
408	130 135 140		
411	Leu Leu Lys Gly Ser Leu Leu Phe Thr Ala Gly Pro Leu Glu Glu		
412	145 150 155 160		
415	Arg Phe Gly Ser Pro Ala Phe Ser Gly Ile Ser Arg Leu Thr Trp Leu		
416	165 170 175		
419	Val Ser Leu Phe Gly Glu Leu Ser Leu Val Ser Ala Thr Leu Glu Glu		
420	180 185 190		
423	Arg Lys Glu Asp Gln Tyr Met Lys Met Thr Val Cys Leu Glu Thr Glu		
424	195 200 205		
427	Lys Lys Ser Pro Leu Ser Trp Ile Glu Glu Lys Gly Pro Gly Leu Lys		
428	210 215 220		
431	Arg Asn Arg Tyr Leu Ser Phe His Phe Lys Ser Gly Ser Leu Glu Asn		
432	225 230 235 240		
435	Val Pro Asn Val Gly Val Asn Lys Asn Ile Phe Leu Lys Asp Gln Asn		
436	245 250 255		
439	Ile Phe Val Gln Lys Leu Leu Gly Gln Phe Ser Glu Lys Glu Leu Ala		
440	260 265 270		
443	Ala Glu Lys Lys Arg Ile Leu His Cys Leu Gly Leu Ala Glu Glu Ile		
444	275 280 285		
447	Gln Lys Tyr Cys Cys Ser Arg Lys		
448	290 295		

VERIFICATION SUMMARY

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Input Set : N:\efs\10584886_efs\Sequence_List_176_61623.txt
Output Set: N:\CRF4\11092006\J584886.raw

L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:29 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (1) SEQUENCE: